# SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

5			( )	A) LI	ENGT	H: 1:	277 l	oase	pai	rs								
			( I	B) T	YPE:	nuc.	leic	acio	d									
			((	C) Si	ranı	DEDNI	ESS:	both	n									
			(1	D) T(	OPOL	OGY:	line	ear										
10		(ii)	) MO]	LECUI	LE T	YPE:	CDN	Ą										
		(ix)	) FE	ATURI	Ξ:													
			(2	A) NA	AME/I	KEY:	CDS											
ļ			( !	B) LO	OCAT:	ION:	1	1275										
15																		
		(xi)	) SE	QUENC	CE DI	ESCR.	IPTI	ON: S	SEQ :	ID NO	0:1:				•			
	ΔTG	GTC	CDD	ΔͲር	CTG	CTG	ጥጥር	ACA	AGA	Δጥጥ	ርሞር	TTG	GTG	GGC	TTC	ATC		48
· .						Leu												- 17
20	1				5				5	10				- 2	15			
	TGC	GCT	CTT	TTA	GTC	TCC	TCT	GGG	CTG	ACT	TGT	GGA	CCA	GGC	AGG	ĠGC		96
	Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly		
				20					25					30				
25																		
	ATT	GGA	AAA	AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCG	TTA	GCC	TAT	AAG	•	144
	Ile	Gly	_	Arg	Arg	His	Pro		Lys	Leu	Thr	Pro		Ala	Tyr	Lys		
			35					40					45					
30	CNC	ጥጥጥ	አ ጥጥ	CCC	አለጥ	GTG	GCA	GAG	AAC	ACC.	СТА	GGG	GCC	ΔСΤ	GGA	ΔCΔ		192
50						Val												102
	0111	50	110	210			55	0_0	2,0		200	60		552	V-1	; <u>5</u>		
	TAT	GAA	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAG	AGA	TTT	AAA	GAA	CTA	ACC		240
35	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr.		
	65					70					75					80		
						GAC												288
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly		

GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly GAC CGC GTG CTG GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC 

	Phe	Leu	Thr	Phe	Leu 245	Asp	Arg	Met	Asp	Ser 250	Ser	Arg	Lys	Leu	Phe 255	Tyr	
5					CGG Arg												816
10	-				GTG Val												864
15					CAG Gln												912
13					CTG Leu												960
20					TCA Ser 325												1008
25					GGC Gly												1056
30					GAG Glu												1104
					CAG Gln												1152
35					GCC Ala												1200
	CTC	CTC	TAC	CGC	ATC	GGC	AGC	TGG	GTG	CTG	GAT	GGT	GAC	GCG	CTG	CAT	1248

	Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His	
					405					410					415		
				ATG						TG							1277
5	Pro	Leu	Gly	Met	Val	Ala	Pro	Ala									
				420					425								
	(2)	TNF	ORMAC	LION	FOR	SEO	ו מד	NO:2	•								
10	(2)	1111		1 2 0 11	LOIK	252	10.		•								
		(i)	) SEC	QUENC	CE C	HARAG	CTER	ISTIC	CS:								
				- A) L!						rs							
			( I	3) T	YPE:	nuc	leic	acio	d								
			((	C) S	rani	DEDNI	ESS:	botl	h								
15			( I	) T(	OPOL	OGY:	line	ear									
		(ii)	MO]	LECUI	LE T	YPE:	cDNZ	J.									
					_												
20		(lx)		ATURI		zev.	CDC										
20				A) NA B) L(				1191									
			( )	J, D.	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		<b></b>										
		(xi)	SE	QUEN	CE DI	ESCR	IPTIO	ON: S	SEQ :	ID NO	0:2:						
25	ATG	GCT	CTG	CCG	GCC	AGT	CTG	TTG	CCC	CTG	TGC	TGC	TTG	GCA	CTC	TTG	48
	Met	Ala	Leu	Pro	Ala	Ser	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu	
	1				5					10					15		
20											CGA						96
30	Ala	Leu	Ser		GIn	Ser	Cys	GTA	Pro 25	GTA	Arg	GTA	Pro	30	GIY	Arg	
				20					23					30			
	CGG	CGT	TAT	GTG	CGC	AAG	CAA	СТТ	GTG	ССТ	CTG	СТА	TAC	AAG	CAG	ттт	144
											Leu						
35	,	_	35		_	_		40					45	_			
	GTG	CCC	AGT	ATG	CCC	GAG	CGG	ACC	CTG	GGC	GCG	AGT	GGG	CCA	GCG	GAG	192
	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
		50					55					60					

	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGC	TTC	CGG	GAC	CTC	GTA	CCC	AAC	240
	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
	65					70					75					80	
5																	
	TAC	AAC	CCC	GAC	ATA	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	288
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
					85					90					95		
10				ACA													336
	Arg	Leu	мет	Thr	GLU	Arg	Cys	гÀг		Arg	vaı	Asn	Ala		Ата	.iie	
				100					105					110			
	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	СТА	CGT	GTG	АСТ	GAA	GGC	384
15				Asn													
			115			-		120		,		,	125			1	
	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
20		130					135					140					
	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gl.y	
	145					150					155					160	
25																	
				CGC													528
	Leu	Leu	Ala	Arg		Ala	Val	Glu	Ala	-	Phe	Asp	Trp	Val	-	Tyr	
					165					170					175		
30	CAC	TCC	CCC	א א כי	CAC	<b>አ</b> ጥሮ	CAC	CTIA	TCC	СТС	71 71 71 T	ССТ	CAT	NNC	TIC N	CTC	576
50				AAC Asn													5/6
	Giu	261	Alg	180	1113	116	1113	vai	185	vaı	ъуs	Ala	дор	190	261	пец	
				100					105					150			
	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	. 624
35				Ala													
			195		_	_	-	200		-			205				
	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	

		210					215					220						
	CTA	СТС	GCC	GCT	СДТ	GCA	GCG	GGC	CGA	GTG.	СΤΔ	CCC	ACG	$CC\Delta$	GTG.	ርፕር		720
				Ala														, 20
5	225	БСС	1114	1114	710P	230		OL y	9	• • • •	235			110		240		
J	220					200												
	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG		768
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val		
					245					250					255			
10																		
	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG		816
	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu		
				260					265					270				
15	GTG	ттС	GCT	GCT	CGC	GGG	CCA	GCG	ССТ	GCT	CCA	GGT	GAC	արար	GCA	CCG		864
10				Ala														
			275		5	1		280				2	285					
	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC		912
20	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly		
		290					295					300						
	GGG	GAC	GCG	CTC	CAG	CCG	GCG	CGC	GTA	GCC	CGC	GTG	GCG	CGC	GAG	GAA		960
	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu		
25	305					310					315					320		
	GCC	GTG	GGC	GTG	TTC	GCA	CCG	CTC	ACT	GCG	CAC	GGG	ACG	CTG	CTG	GTC	]	1008
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val		
					325					330					335			
30																		0.5.4
				CTC													]	1056
	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr		Val	Leu	GLu	Ser		GIn	Trp		
				340					345					350				
35	GCC	CAC	CGC	GCC	TTC	GCC	CCT	TTG	CGG	CTG	CTG	CAC	GCG	CTC	GGG	GCT	1	104
	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala		
			355					360					365					
	CTG	CTC	CCT	GGG	GGT	GCA	GTC	CAG	CCG	ACT	GGC	ATG	CAT	TGG	TAC	TCT	1	.152
										6/61								

	Leu	Leu 370	Pro	Gly	Gly	Ala	Val 375	Gln	Pro	Thr	Gly	Met 380	His	Trp	Tyr	Ser	
5				TAC Tyr									TG				1190
10	(2)		SE(	TION  QUENC  A) LI  B) T	CE CI ENGTI	HARA(	CTERI 281 k	ISTI( pase	CS: pai:	rs		·					
15		(ii)	1)	C) STO	TRANI OPOLO	DEDNI	ESS: line	botl ear									
20			( <i>I</i>	ATURI A) NA B) LO	AME/I	ION:	1										
25		(xi)	SE(	QUENC	CE DE	ESCRI	IPTI(	ON: S	SEQ :	ID NO	0:3:						
				GCC Ala													48
30				CTT Leu 20													96
35				AGC Ser													144
				TTC Phe													192

7/61

		50					55					60					
	GGG	CGC	ТАС	GAA	GGC	AAG	АТС	GCG	CGC	AGC	тст	GAG	CGC	ттс	ΔΔΔ	GAG	240
								Ala									
5	65	9	- 1 -	0	07	70			9	-	75		9		-1-	80	
	CTC	ACC	CCC	AAC	TAC	AAT	CCC	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	288
	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	
					85					90					95		
10																	
	ACG	GGT	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGT	CTG	AAC	336
	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	
				100					105					110			
15	TCA	CTG	GCC	ATC	TCT	GTC	ATG	AAC	CAG	TGG	CCT	GGT	GTG	AAA	CTG	CGG	384
	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
			115					120					125				
								GAT									432
20	Val		Glu	Gly	Arg	Asp		Asp	Gly	His	His		Glu	Glu	Ser	Leu	
		130					135					140					
		DO 20 CO	C D C	000	000	666	C.T.C	C T III	7.00	7.00	7.00	m $\sim$ $^{3}$	C n C	CCM	CAC	CCI	400
								GAT									480
25		Tyr	GIU	стХ	Arg		vai	Asp	ire	Thr		Ser	Asp	Arg	Asp		-
25	145					150					155					160	
	ልልጥ	AAC	ጥልጥ	GGA	СТС	СТС	GCG	CGC	ጥጥΔ	GCA	GTG	GAG	GCC	GGC	ጥጥር	GAC	528
								Arg									520
	71311	цуз	ТУТ	Ory	165	пси	nii	711 G	ЦСИ	170	Vai	Giu	711. CI	Gry	175	1155	
30					100					1,0					1.0		
•	TGG	GTG	ТАТ	TAC	GAG	TCC	AAG	GCC	CAC	GTG	CAT	TGC	TCT	GTC	AAG	TCT	576
								Ala									
	<u></u>			180					185			3		190	- 3		
35	GAG	CAT	TCG	GCC	GCT	GCC	AAG	ACA	GGT	GGC	TGC	TTT	CCT	GCC	GGA	GCC	624
	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
			195					200					205				
	CAG	GTG	CGC	СТА	GAG	AAC	GGG	GAG	CGT	GTG	GCC	CTG	TCA	GCT	GTA	AAG	672

	Gln	Val 210	Arg	Leu	Glu	Asn	Gly 215	Glu	Arg	Val	Ala	Leu 220	Ser	Ala	Val	Lys	
	CCA	GGA	GAC	CGG	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	ACC	CCC	ACC	TTC	720
5	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
	225					230					235					240	
	AGT	GAT	GTG	CTT	ATT	TTC	CTG	GAC	CGC	GAG	CCA	AAC	CGG	CTG	AGA	GCT	768
	Ser	Asp	Val	Leu		Phe	Leu	Asp	Arg		Pro	Asn	Arg	Leu	_	Ala	
10					245					250					255		
-	TTC	CAG	GTC	ATC	GAG	ACT	CAG	GAT	CCT	CCG	CGT	CGG	CTG	GCG	CTC	ACG	816
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
				260					265					270			
15	CCT	ccc	CAC	<b>C</b> TIC	CTIC	mm¢	zy en m	CCC	CNC	7. 7. TT	C A TI	7.07	CNN	CCA	CCA	CCC	0.54
												ACA Thr					864
	110	1110	275	шси	пси	1110	110	280	715P	1,511	1120	1111	285	110	71.10	1114	
•																	
20	CAC	TTC	CGG	GCC	ACA	TTT	GCC	AGC	CAT	GTG	CAA	CCA	GGC	CAA	TAT	GTG	912
	His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
		290					295					300					
•																	0.50
25												CGG					960
23	305	val	ser	GIY	vaı	310	СТУ	ьeu	GIII	PLO	315	Arg	Val	нта	Ala	320	
	303					310					313					320	
	TCC	ACC	CAC	GTG	GCC	CTT	GGG	TCC	TAT	GCT	CCT	CTC	ACA	AGG	CAT	GGG	1008
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
30					325					330					335		
												TTT					1056
	Thr	Leu	Val		Glu	Asp	Val	Val		Ser	Cys	Phe	Ala		Val	Ala	
35				340					345					350			
55	GAC	CAC	САТ	CTG	GCT	CAG	ፐፐር	GCC	ጥጥር	ፐርር	CCC	CTG	CGA	СТС	ጥጥጥ	CCC	1104
												Leu					1101
	•		355					360	_	•			365				

	AGT TTG GCA TGG GGC AGC TGG ACC CCA AGT GAG GGT GTT CAC TCC TAC	1152
	Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr	
	370 375 380	
5	CCT CAG ATG CTC TAC CGC CTG GGG CGT CTC TTG CTA GAA GAG AGC ACC	1200
	Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr	
	385 390 395 400	
10	TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG	1253
10	Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410	
	405 410	
	CCCTCCTGGA ACTGCTGTGC GTGGATCC	1281
	decreers. Nercerares strontes	1201
15		
	(2) INFORMATION FOR SEQ ID NO:4:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1313 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: both	
	(D) TOPOLOGY: linear	
	( ) NOT ECHT E TUDE . DVD	
25	(ii) MOLECULE TYPE: cDNA	
23		
	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 11314	
30		,
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	ATG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG	48
35	Met Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser	
	1 5 1Ó 15	
		_
	CTG CTG GTG TGC CCC GGG CTG GCC TGT GGG CCC GGC AGG GGG TTT GGA	96
	Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly	

				20					25					30			
	AAG	AGG	CGG	CAC	CCC	AAA	AAG	CTG	ACC	ССТ	TTA	GCC	TAC	AAG	CAG	TTT	144
	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	
5			35					40					45				
	ATT	CCC	AAC	GTA	GCC	GAG	AAG	ACC	СТА	GGG	GCC.	AGC	GGC	AGA	TAT	GAA	192
	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	
		50					55					60					
10																	
											AAG						240
	_	Lys	Ile	Thr	Arg		Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro		
	65					70					75					80	
15	TAC	AAC	CCC	GAC	ATC	ATA	ттт	AAG	GAT	GAG	GAA	AAC	ACG	GGA	GCA	GAC	288
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	
					85					90					95		
	CGG	CTG	ATG	ACT	CAG	.AGG	TGC	AAA	GAC	AAG	TTA	AAT	GCC	TTG	GCC	ATC	336
20	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
				100					105					110			
	m C m	cmc	7 m.c	7 7 C	CAC	mcc	CCT	CCN	CMC	3.00	CTC	CCA	CTC	7.00	CAC	CCC	201
											CTG						384
25	ser	vaı	115	ASII	GIII	пр	FIO	120	vaı	Ary	Leu	Arg	125	1111	GIU	GIY	•
23			113					120					123				
	TGG	GAT	GAG	GAC	GGC	CAT	CAT	TCA	GAG	GAG	TCT	CTA	CAC	TAT	GAG	GGT	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
		130					135					140					
30																	
											GAC -						480
	_	Ala	Val	Asp	Ile		Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	<del>-</del>	
	145				٠	150					155					160	•
35	ATG	CTG	GCT	CGC	CTG	GCT	GTG	GAA	GCA	GGT	TTC	GAC	TGG	GTC	TAC	TAT	528
	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170					175		
	GAA	ፐርር	ддд	GCT	CAC	АТС	CAC	ፐርፐ	тст	GTG	AAA	GCA	GAG	AAC	TCC	GTG	576
	O. 11 1	100		001	00		~ <del>·</del>			010			O. 10			<del>-</del>	

	Glu	Ser	Lys	Ala 180	His	Ile	His	Cys	Ser 185	Val	Lys	Ala	Glu	Asn 190	Ser	Val		
	GCG	GCC	AAA	TCC	GGC	GGC	TGT	TTC	CCG	GGA	TCC	GCC	ACC	GTG	CAC	CTG	6:	2.4
5	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu		
			195					200					205					
	GAG	CAG	GGC	GGC	ACC	AAG	CTG	GTG	AAG	GAC	TTA	CGT	CCC	GGA	GAC	CGC	6	72
						Lys												
10		210					215					220						
			•															
						GAC											7:	20
		Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu		Tyr	Ser	Asp	Phe			
15	225					230					235					240		
13	ACC	TTC	CTG	GAC	CGC	GAC	GAA	GGC	GCC	AAG	AAG	GTC	TTC	TAC	GTG	ATC	7	68
	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile		
					245					250					255			
			7															
20						CGC											8	16
	Glu	Thr			Pro	Arg	Glu	Arg		Leu	Leu	Thr	Ala		His	Leu		
				260					265					270				
	CTC	TTC	GTG	GCG	CCG	CAC	AAC	GAC	TCG	GGG	CCC	ACG	CCC	GGG-	CCA	AGC	8	64
25	Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser		
			275					280					285					
	000	am o	mmm	000	7.00	000	ama	000	000	000	an a	000	OTT C	m » C	c.m.c.	C.III.C	0.7	
						CGC Arg											9.	12
30	AIa	290	rne	АТА	Ser	ALG	295	ALG	110	Gry	GIII	300	Vai	ı yı	vai	var		
	GCT	GAA	CGC	GGC	GGG	GAC	CGC	CGG	CTG	CTG	CCC	GCC	GCG	GTG	CAC	AGC	96	60
	Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser		
	305					310					315		·			320		
35																		
	_					GAG											100	80
	vaı	Thr	ьeu	Arg	G1u 325	Glu	GIU	Ата	σтλ	330	Tyr	Ата	Pro	ьeu	335	нта		
					J Z J					550					555			

35

	CAC	GGC	ACC	ATT	CTC	ATC	AAC	CGG	GTG	CTC	GCC	TCG	TGC	TAC	GCT	GTC	1056
	His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	
				340					345					350			
5							GCA										1104
	Ile	Glu		His	Ser	Trp	Ala		Arg	Ala	Phe	Ala		Phe	Arg	Leu	
			355					360					365				
	666	CAC	CCC	CTI C	CTC	ccc	GCG	CTC	CCA	CCC	CCC	CCC	7.00	CAC	CCC	CCC	1152
10							Ala										1132
10	Ата	370	Ala	ьеu	reu	Ата	375	ьeu	Ala	FIO	Ата	380	1111	Asp	ЭТУ	GIY	
		370					373					300					
	GGC	GGG	GGC	AGC	ATC	ССТ	GCA	GCG	CAA	TCT	GCA	ACG	GAA	GCG	AGG	GGC	1200
	Glv	Glv	Glv	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly	•
15	385		_			390					395				_	400	
	GCG	GAG	CCG	ACT	GCG	GGC	ATC	CAC	TGG.	TAC	TCG	CAG	CTG	CTC	TAC	CAC	1248
	Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His	
					405					410					415		
20											•						
	ATT	GGC	ACC	T'GG	CTG	TTG	GAC	AGC	GAG	ACC	ATG	.CAT	CCC.	TTG	GGA	ATG	1296
	Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met	
				420					425					430			
25				TCC		TG											1313
	Ala	Val	_	Ser	Ser												
			435														

## 30 (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

			( )	A) N	AME/I	KEY:	CDS										
			( ]	B) L	OCAT:	ION:	1	1257									
5																	
		(xi	) SEC	QUEN	CE DI	ESCR	IPTI	: : NC	SEQ :	ID NO	0:5:						
										GTG							48
10		Arg	Leu	Leu		Arg	vaı	Leu	Leu	Val	Ser	Leu	Leu	Thr		Ser	
	1				5					10					15		
	TTG	GTG	GTG	TCC	GGA	CTG	GCC	TGC	GGT	CCT	GGC	AGA	GGC	TAC	GGC	AGA	96
	Leu	Val	Val	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Tyr	Gly	Arg	
15				20					25					30			
										CTC							144
	Arg	Arg		Pro	Lys	Lys	Leu		Pro	Leu	Ala	Tyr		Gln	Phe	Ile	
20			35					40					45				
20	CCT	<b>አ</b> አኒጥ	CTC	CCC	CAC	አ አ C	N.C.C	ጥጥለ	CCC	CCC	N.C.C	CCC	እሮአ	<b>ጥ</b> አ ር	CNC	CCC	192
										GCC Ala							192
•	110	50	va.	ATG	Gia	цуз	55	пец	GLY	ALG	Ser	60	Arg	ıyı	010	GLY	
25	AAG	ATA	ACG	CGC	AAT	TCG	GAG	AGA	ттт	AAA	GAA	CTT	ACT	CCA	AAT	TAC	240
	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65					70					75					80	
	AAT	CCC	GAC	ATT	ATC	TTT	AAG	GAT	GAG	GAG	AAC	ACG	GGA	GCG	GAC	AGG	288
30	Asn	Pro	Asp	Ile		Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala		Arg	
					85					90					95		
	CTTC	א חור	7 C 7	CAC	7.07	mcc.	7. 7. 7.	CAC	7 7 C	CTG	7 7 C	mcc.	CTC	ccc	7. T.C	m.c.m	336
										Leu							336
35	neu	Mec	1111	100	ALG	СуЗ	пуз	АЗР	105	пец	ASII	Ser	ьец	110	116	561	
33				100					100								
	GTA	ATG	AAC	CAC	TGG	CCA	GGG	GTT	AAG	CTG	CGT	GTG	ACA	GAG	GGC	TGG	384
										Leu							
			115					120					125				

	GAT	GAG	GAC	GGT	CAC	CAT	TTT	GAA	GAA	TCA	CTC	CAC	TAC	GAG	GGA	AGA	432
	Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
		130					135					140					
5																	
	GCT	GTT	GAT	ATT	ACC	ACC	TCT	GAC	CGA	GAC	AAG	AGC	AAA	TAC	GGG	ACA	480
	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr	
	145					150					155					160	
10												TGG					528
	Leu	Ser	Arg	Leu		Val	Glu	Ala	Gly		Asp	Trp	Val	Tyr		Glu	
					165					170					175		
	maa	70.70	666	C T C	7 mm	C D III	nic.c	m.c.m	CITIC	70 70 70	CCA	C D D	70.70.00	mcc.	CMM	CCI	E 7 6
15												GAA					576
13	ser	гуѕ	Ата	180	TTE	urz	Cys	ser	185	пур	Αiα	Glu	ASII	190	vaı	Ala	
				100					105					150			
	GCG	AAA	TCT	GGG	GGC	TGT	TTC	CCA	GGT	TCG	GCT	CTG	GTC	TCG	CTC	CAG	624
												Leu					
20		-	195	_		•		200	•				205				
	GAC	GGA	GGA	CAG	AAG	GCC	GTG	AAG	GAC	CTG	AAC	CCC	GGA	GAC	AAG	GTG	672
	Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	
		210					215					220					
25																	
	CTG	GCG	GCA	GAC	AGC	GCG	GGA	AAC	CTG	GTG	TTC	AGC	GAC	TTC	ATC	ATG	720
	Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met	
	225					230					235					240	
30					GAC									GTC			768
	Phe	Thr	Asp	Arg	_	Ser	Thr	Thr	Arg		Val	Phe	Tyr	Val		Glu	
					245					250					255		
	7.00	C 7 7	C D D	CCC	C TR TR	CDD	7 7 C	n m c	7.00	CITIC	7.00	CCC	CCIII	CAC	CMC	COUR	016
35												GCC Ala					816
33	THE	GIII	GIU	260	Val	GIU	гус	тте		ьeu	TilL	Ата	Ата	270	ьеи	rea	
				200					265					2/0			
	ጥጥጥ	GTC	СТС	GAC	AAC	тса	ACG	GAA	СДТ	СТС	CAC	ACC	ΔТС	ACC	GCC	GCG	864
												Thr					004
				P					p		0						

			275					280					285				
												ATG					912
5	Tyr	Ala 290	Ser	Ser	Val	Arg	Ala 295	Gly	Gln	Lys	Val	Met 300	Val	Val	Asp	Asp	
												ATA Ile					960
10	305	,			-,,-	310					315		-1-			320	
												GGG Gly					1008
					325					330					335		,
15												GAG Glu					1056
	GCG	САТ	TTG		TTC	GCG	CCC	GCC		СТС	ТАТ	TAT	TAC		тса	TCA	1104
20												Tyr					
	TTC	CTG	TCC	CCC	AAA	ACT	CCA	GCA	GTC	GGT	CCA	ATG	CGA	CTT	TAC	AAC	1152
25	Phe	Leu 370	Ser	Pro	Lys	Thr	Pro 375	Ala	Val	Gly	Pro	Met 380	Arg	Leu	Tyr	Asn	
												CAT His					1200
30		Cmm	mm.c	CAC	n.c.c		A TIC	C TT TT	C A M	CCM		ccc	7 m.c	m C A	CMA		1240
												GGG Gly					1248
35	TCA	AGC	TG														1256
	Ser	Ser															

(2) INFORMATION FOR SEQ ID NO:6:

5		(i)	(1 (1	A) L1 B) T' C) S'	CE CI ENGTI YPE: IRANI OPOLO	H: 1 nuc DEDNI	425 ) leic ESS:	oase acio sino	pai: d	rs								
10		(ii	) MO:	LECUI	LE T	YPE:	cDN	Δ										
15		(ix)	( )	•	E: AME/I OCATI			1425										
		(xi)	) SE	QUEN	CE DI	ESCR:	IPTI(	: NC	SEQ :	ID NO	0:6:							
20					GCG Ala													48
25					GGA Gly												:	96
20					AAA Lys													144
30					GAG Glu													192
35					AAC Asn												:	240
	AAC	ccc	GAC	ATC	ATA	TTT	AAG	GAT	GAA	GAA	AAC	ACC	GGA	GCG	GAC	AGG	:	288

	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
5						TGT Cys											336
10						CCA Pro											384
						CAC His											432
15						ACG Thr 150											480
20						GTG Val										GAG Glu	528
25						CAC His											576
30						TGC Cys											624
						CTG Leu											672
35						CAG Gln 230											720

	TTC	CTG	GAC	CGC	GAC	GAC	GGC	GCC	AAG	AAG	GTC	TTC	TAC	GTG	ATC	GAG	768
	Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val		Glu	
					245					250					255		
5	ACG	CGG	GAG	CCG	CGC	GAG	CGC	CTG	CTG	CTC	ACC	GCC	GCG	CAC	CTG	CTC	816
	Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	
				260					265					270			
10								TCG									864
10	rne	vaı	275	PIO	птэ	ASII	Asp	Ser 280	АІа	1111	СТУ	GIU.	285	GIU	АІА	Ser	
	TCG	GGC	TCG	GGG	CCG	CCT	TCC	GGG	GGC	GCA	CTG	GGG	CCT	CGG	GCG	CTG	912
	Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu	
15		290					295					300					
	ጥጥር	GCC	AGC	CGC	GTG	CGC	CCG	GGC	CAG	CGC	GTG	ТАС	GTG	GTG	GCC	GAG	960
								Gly									300
	305		- %	,		310		_		,	315	,				320	
20											*	•					
	CGT	GAC	GGG	GAC	CGC	CGG	CTC	CTG	CCC	GCC	GCT	GTG	CAC	AGC	GTG	ACC	1008
	Arg	'Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro		Ala	Val	His	Ser		Thr	
					325					330					335		
25	СТА	AGC	GAG	GAG	GCC	GCG	GGC	GCC	TAC	GCG	CCG	CTC.	ACG	GCC	CAG	GGC	1056
								Ala									
				340					345					350			
20								CTG									1104
30	Thr	iie	355	iie	Asn	Arg	vaı	Leu 360	Ата	Ser	Cys	Tyr	365	vaı	iie	GIU	
		,	333					300					303				
	GAG	CAC	AGC	TGG	GCG	CAC	CGG	GCC	TTC	GCG	CCC	TTC	CGC	CTG	GCG	CAC	1152
	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His	
35		370					375					380					
															25-	<b></b>	400 <del>-</del>
								CCC									1200
	385	теп	ren	нта	нта	390	Ата	Pro	Ата	Arg	395	АЅР	Arg	атА	ату	400	
	505					550										100	

	AGC	GGC	GGC	GGG	GAC	CGC	GGG	GGC	GGC	GGC	GGC	AGA	GTA	GCC	CTA	ACC	1248
	Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr	
					405					410					415		
5																	
	GCT	CCA	GGT	GCT	GCC	GAC	GCT	CCG	GGT	GCG	GGG	GCC	ACC	GCG	GGC	ATC	1296
	Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile	
				420					425					430			
10	CAC	TGG	TAC	TCG	CAG	CTG	CTC	TAC	CAA	ATA	GGC	ACC	TGG	CTC	CTG	GAC	1344
	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp	
								440					445				
			435					440					440				
			435					440					.4.4.3				
	AGC	GAG		CTG	CAC	CCG	CTG		ATG	GCG	GTC	AAG		AGC	NNN	AGC	1392
15			GCC					GGC			GTC Val		TCC				1392
15			GCC					GGC					TCC				1392
15		Glu	GCC				Leu	GGC				Lys	TCC				1392
15	Ser	Glu 450	GCC Ala	Leu	His		Leu 455	GGC Gly	Met	Ala	Val	Lys	TCC				1392 1425
15	Ser CGG	Glu 450 GGG	GCC Ala	Leu GGG	His GGA	Pro GGG	Leu 455 GCG	GGC Gly	Met GAG	Ala GGG	Val GCC	Lys	TCC				
15	Ser CGG	Glu 450 GGG	GCC Ala	Leu GGG	His GGA	Pro	Leu 455 GCG	GGC Gly	Met GAG	Ala GGG	Val GCC	Lys	TCC				
	Ser CGG Arg	Glu 450 GGG	GCC Ala	Leu GGG	His GGA	Pro GGG Gly	Leu 455 GCG	GGC Gly	Met GAG	Ala GGG	Val GCC Ala	Lys	TCC				

(2) INFORMATION FOR SEQ ID NO:7:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1622 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
- 30 (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
- 35 (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 51..1283

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	CAT	CAGC	CCA (	CCAG	GAGA(	CC TO	CGCC	CGCC	G CT	CCCC	CGGG	CTC	CCCG	GCC I	ATG '	тст	56
														1	Met :	Ser	
5															1		
	CCC	GCC	CGG	CTC	CGG	CCC	CGA	CTG	CAC	TTC	TGC	CTG	GTC	CTG	TTG	CTG	104
	Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu	Leu	Leu	
			5					10					15				
10																	
	CTG	CTG	GTG	GTG	CCC	GCG	GCA	TGG	GGC	TGC	GGG	CCG	GGT	CGG	GTG	GTG	152
	Leu	Leu	Val	Val	Pro	Ala	Ala	Trp	Gly	Cys	Gly	Pro	Gly	Arg	Val	Val	
		20					25					30					
			٠														
15	GGC	AGC	CGC	CGG	CGA	CCG	CCA	CGC	AAA	CTC	GTG	CCG	CTC	GCC	TAC	AAG	200
	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	l'yr	Lys	
	35					40					45					50	
	CAG	TTC	AGC	CCC	AAT	GTG	CCC	GAG	AAG	ACC	CTG	GGC	GCC	AGC	GGA	CGC	248
20	Gln	Phe	Ser	Pro	Asn	Val	Pro	Gl.u	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
					55					60					65		
	TAT	GAA	GGC	AAG	ATC	GCT	CGC	AGC	TCC	GAG	CGC	TTC	AAG	GAG	CTC	ACC	296
	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	•
25				70					75					80			
	CCC	AAT	TAC	AAT	CCA	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	ACA	GGC	344
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
			85					90					95				
30																	
	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGC	CTG	AAC	TCG	CTG	392
	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	Ser	Leu	
		100					105					110					
35	GCT	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGT	GTG	AAG	CTG	CGG	GTG	ACC	440
	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
	115					120					125					130	
	GAG	GGC	TGG	GAC	GAG	GAC	GGC	CAC	CAC	TCA	GAG	GAG	TCC	CTG	CAT	TAT	488
									,	21/61							

	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
					135					140					145		
		000	666	000	Cm.c	67.6	7 M.C	7.00	7.07	m $\curvearrowright$ n	C D C	020	C T C	000	70.70	7 7 C	<b>5</b> 26
5						GAC											536
5	GIU	GTA	Arg	150	Val	Asp	тте	1111	155	ser	ASP	Arg	ASP	160	ASII	гАг	
				100					100					100		•	
	TAT	GGA	CTG	CTG	GCG	CGC	TTG	GCA	GTG	GAG	GCC	GGC	ттт	GAC	TGG	GTG	584
	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
10			165					170					175				
	TAT	TAC	GAG	TCA	AAG	GCC	CAC	GTG	CAT	TGC	TCC	GTC	AAG	TCC	GAG	CAC	632
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
		180					185				•	190					
15	mac.	666	CCT	ccc	ח ח כי	7.00	666	666	mcc	mmc	CCM	000	C C N	ccc	CAC	C III N	600
						ACG Thr											680
	195	AIG	AIG	ALG	шуз	200	Gry	Gry	СуЗ	1116	205	ALG	OLY	ALG	OIII	210	
	220																
20	CGC	CTG	GAG	AGT	GGG	GCG	CGT	GTG	GCC	TTG	TCA	GCC	GTG	AGG	CCG	GGA	728
	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
					215					220					225		
						ATG											776
25	Asp	Arg	Val		Ala	Met	Gly	Glu		Gly	Ser	Pro	Thr		Ser	Asp	
				230					235					240			
	GTG	ርሞር	Δυπ	ጥጥር	СТС	GAC	CGC	GAG	CCC	CAC	AGG	СТС	AGA	GCC	ጥጥር	CAG .	824
						Asp											021
30			245			•	_	250			_		255				
	GTC	ATC	GAG	ACT	CAG	GAC	CCC	CCA	CGC	CGC	CTG	GCA	CTC	ACA	CCC	GCT	872
	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	
		260					265					270					
35										•							
						GCT											920
		Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr		Pro	Ala	Ala	Arg		
	275					280					285					290	

	CGG	GCC	ACA	TTT	GCC	AGC	CAC	GTG	CAG	CCT	GGC	CAG	TAC	GTG	CTG	GTG	968
	Arg	Ala	Thr	Phe	Ala 295	Ser	His	Val	Gln	Pro 300	Gly	Gln	Tyr	Val	Leu 305	Val	
5															TCT Ser		1016
	AIA	GIÀ	vai	310	GIY	Беа	GIII	110	315	Arg	vai	Ala	ALG	320	Ser	1111	
															ACA		1064
10	His	Val	A1a 325	Leu	GIY	Ala	Tyr	330	Pro	Leu	Thr	Lys	335	GTÀ	Thr	Leu	
	GTG	GTG	GAG	GAT	GTG	GTG	GCA	TCC	TGC	TTC	GCG	GCC	GTG	GCT	GAC	CAC	1112
15	Val	Val 340	Glu	Asp	Val	Val	Ala 345	Ser	Cys	Phe	Ala	Ala 350	Val	Ala	Asp	His	
															AGC		1160
	Hi.s 355	Leu	Ala	Gln	Leu	Ala 360	Phe	Trp	Pro	Leu	Arg 365	Leu	Phe	His	Ser	Leu 370	
20																	
															CCC		1208
	Ala	Trp	Gly	Ser	375	Thr	Pro	Gly	Glu	Gly 380	Va!	His	Trp	Tyr	Pro 385	Gln	
25	CTG	CTC	TAC	CGC	CTG	GGG	CGT	CTC	CTG	СТА	GAA	GAG	GGC	AGC	TTC	CAC	1256
	Leu	Leu	Tyr	Arg 390	Leu	Gly	Arg	Leu	Leu 395	Leu	Glu	Glu	Gly	Ser 400	Phe	His	
	CCA	CTG	GGC	ATG	TCC	GGG	GCA	GGG	AGC	TGA	AAGGA	ACT (	CCAC	CGCT	GC		1303
30	Pro	Leu	Gly 405	Met	Ser	Gly	Ala	Gly 410	Ser								
	ССТО	CCTGG	GAA (	CTGCT	rgtac	CT GO	GTC	CAGA	A GCC	СТСТС	CAGC	CAGO	GAGG	GAG (	CTGGC	CCTGG	1363
35	AAGO	GACC	CTG A	AGCTO	GGGG	SA CA	ACTGO	GCTCC	C TGC	CCATO	CTCC	TCTO	GCCA:	rga <i>i</i>	AGATA	ACACCA	1423
	TTGA	AGACI	TTG A	ACTGO	GCA	AC AC	CCAGO	CGTCC	c ccc	CACCO	CGCG	TCGT	GGT	GTA (	GTCAT	AGAGC	1483
	TGCF	AAGCI	rga (	GCTGC	GCGAC	G GC	SATGO	STTGI	TGF	ACCCC	СТСТ	CTCC	CTAGA	AGA (	CCTTC	SAGGCT	1543

	GGC	ACGG(	CGA (	CTCC	CAAC!	rc ac	GCCT	GCTCI	CAC	CTAC	GAGT	TTTC	CATA	CTC 7	rgcc'	гссссс	1603
	ATT	GGGA	GGG (	CCCA:	rtcc												1622
5	(2)	INF	ORMA'	rion	FOR	SEQ	ID ì	10:8:									
10		(i.)	( ) ( )	A) LE B) T' C) S'	ENGTI YPE: FRANI	H: 11 nucl	191 k Leic	STIC pase acic both ear	pai:	rs							
15		(ii)	) MO1	LECUI	LE T	YPE:	cDNA	Ą								٠.	
20			(1	A) NA B) L(	AME/I	ON:	1	L191 ON: S	SEQ I	: ID NO	D:8:						
25	Met	GCT	CTC	CTG	ACC	AAT	СТА	CTG Leu	CCC	TTG Leu	TGC						48
				Ala	CAG			GGG Gly	Pro					Val	GGC		96
30								CTC Leu									144
35	GTG	ccc	35 GGC	GTG	CCA	GAG	CGG	40 ACC	CTG	GGC	GCC	AGT	45 GGG	CCA	GCG	GAG	192
	Val	Pro 50	Gly	Val	Pro	Glu	Arg 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Pro	Ala	Glu	

	GGG	AGG	GTG	GCA	AGG	GGC	TCC	GAG	CGC	TTC	CGG	GAC	CTC	GTG	CCC	AAC		240
	Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn		
	65					70					75					80		
5	TAC	AAC	CCC	GAC	ATC	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGT	GGA	GCC	GAC		288
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp		
					85					90					95			
	CGC	CTG	ATG	ACC	GAG	CGT	TGC	AAG	GAG	AGG	GTG	AAC	GCT	TTG	GCC	ATT		336
10	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile		
				100					105					110				
	GCC	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTG	CGC	CTA	CGA	GTG	ACT	GAG	GGC		384
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly		
15			115					120					125					
	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCT	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC		432
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	-	
		130					135					140						
20																		
														AAG -				480
	_	Ala	Leu	Asp	Ile		Thr	Ser	Asp	Arg		Arg	Asn	Lys	Tyr			
	145					150					155					160		
25	TTG	CTG	GCG	CGC	CTC	GCA	GTG	GAA	GCC	GGC	TTC	GAC	TGG	GTC	TAC	TAC		528
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr		
					165					170					175			
	GAG	TCC	CGC	AAC	CAC	GTC	CAC	GTG	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG		576
30	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu		
				180					185					190				
	GCG	GTC	CGG	GCG	GGC	GGC	TGC	TTT	CCG	GGA	AAT	GCA	ACT	GTG	CGC	CTG		624
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu		
35			195					200					205					
	TGG	AGC	GGC	GAG	CGG	AAA	GGG	CTG	CGG	GAA	CTG	CAC	CGC	GGA	GAC	TGG		672
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp		
		210					215					220						

							CCC Pro			720
5							TCA Ser			768
10							ACG Thr			816
15							GGC Gly			864
20							GTG Val 300			912
÷							GTG Val			960
25							GGG Gly			1008
30							GAG Glu			1056
35							CAC His			1104
					Pro	Gly	ATG Met			1152

		370					375					380					
				TAC									TG				119
5	385	Leu	Leu	Tyr	Arg	390	Ala	Giu	GIU	Leu	395	GIY					
10	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:9	:								
		(i)	) SE	QUEN	CE CI	HARA	CTER	ISTI	CS:				•				
			(2	A) LI	ENGTI	H: 1:	251	base	pai	rs							
			( ]	B) T	YPE:	nuc.	leic	aci	d								
			((	C) Si	ranı	DEDNI	ESS:	bot	h		-						
15			(1	D) T(	OPOLO	OGY:	lin	ear									
		(ii)	) MO	LECUI	LE T	YPE:	cDN	A									
20		(ix)	) FE	ATURI	€:												
			(2	A) NA	AME/I	KEY:	CDS										
			(1	B) LO	OCAT:	ON:	1	1248									
						•											
25		(xi)	) SE	QUENC	CE DI	ESCR:	IPTI	: :NC	SEQ :	ID NO	0:9:						
	ATG	GAC	GTA	AGG	CTG	CAT	CTG	AAG	CAA	ттт	GCT	TTA	CTG	TGT	TTT	ATC	4 8
	Met	Asp	Val	Arg	Leu	His	Leu	Lys	Gln	Phe	Ala	Leu	Leu	Cys	Phe	Ile	
	1				5					10					15		
30																	
	AGC	TTG	CTT	CTG	ACG	CCT	TGT	GGA	TTA	GCC	TGT	GGT	CCT	GGT	AGA	GGT	96
	Ser	Leu	Leu	Leu	Thr	Pro	Cys	Gly		Ala	Cys	Gly	Pro	_	Arg	Gly	
				20					25					30			
35	TAT	GGA	AAA	CGA	AGA	CAC	CCA	AAG	AAA	TTA	ACC	CCG	TTG	GCT	TAC	AAG	144
	Tyr	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	
			35					40					45				
	CAA	TTC	ATC	CCC	AAC	GTT	GCT	GAG	AAA	ACG	СТТ	GGA	GCC	AGC	GGC	AAA	192

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100

	Gln		Ile	Pro	Asn	Val		Glu	Lys	Thr	Leu	-	Ala	Ser	Gly	Lys	
		50					55					60					
	TAC	GAA	GGC	AAA	ATC	ACA	AGG	AAT	TCA	GAG	AGA	TTT	AAA	GAG	CTG	ATT	240
5	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Ile	
	65					70					75					80	
	CCG	AAT	TAT	AAT	CCC	GAT	ATC	ATC	ттт	AAG	GAC	GAG	GAA	AAC	ACA	AAC	288
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Asn	
10					85					90					95		
	CCT	CAC	7,00	CTC	አ ሞ C	N.C.C	አ አ C	CCC	ሞርጥ	<u>አ</u> አር	CAC	NNC	ጥጥለ	א א ידי	TCG	<del>ጥጥ</del> ር	336
	Ala																250
		1.0.5	9	100	1100		-10		105			-1-		110			
15																	
	GCC	ATA	TCC	GTC	ATG	AAC	CAC	TGG	CCC	GGC	GTG	AAA	CTG	CGC	GTC	ACT	384
	Ala	Ile	Ser	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
			115					120					125				
20	C N N	CCC	mcc.	CAM	CAC	C A TO	CCT	CAC	CAT	uru v	$C \Lambda \Lambda$	$C \Lambda \Lambda$	TI COT	መመር	CAC	ייז א ייז	432
20															His		432
•	Olu	130	111	7100	Olu	пор	1.35	11 _ 0	1110	1100	Ola	140	001	LCu		- 1 -	
	GAG	GGA	CGG	GCA	GTG	GAC	ATC	ACT	ACC	TCA	GAC	AGG	GAT	AAA	AGC	AAG	480
25	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	
	145					150					155					160	
	TAT	GGG	ATG	CTA	TCC	AGG	CTT	GCA	GTG	GAG	GCA	GGA	TTC	GAC	TGG	GTC	528
	Tyr	Gly	Met	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
30					165					170					175		
	TAT	TAT	GAA	TCT	AAA	GCC	CAC	ATA	CAC	TGC	TCT	GTC	AAA	GCA	GAA	AAT	576
	Tyr	Tyr	Glu		Lys	Ala	His	Ile		Cys	Ser	Val	Lys		Glu	Asn	
25				180					185					190			
35	ጥሮል	GTG	GCT	GCT	ΔΔΔ	ፐርΔ	GGA	GGA	ሞ <b>ር</b> ሞ	ጥጥጥ	ССТ	GGG	ጥርጥ	GGG	ACG	GTG	624
				Ala													024

		~	~~~									C 7 M	C.M.M.	70 70 70	0.00	000	67.0
												GAT					672
	Thr		Gly	Asp	GLY	Thr	-	гуs	Pro	IIe	Lуs	Asp	Leu	гуs	val	GIY	
		210					215					220					
_	~ ~ ~	~~~		mmc		667	07.6	07.0	7.7.0	007	7 7 01	C TO C	mm 2	7 M 7	7.00	07.0	700
5												GTC					720
	-	Arg	Val	Leu	Ala		Asp	Glu	Lys	GLY		Val	Leu	тте	Ser	-	
	225					230					235					240	
	mmm	N m m	7 m.c	mmm.	א נווי א	CAC	CAC	CAT	CCC	7.07	N.C.C	AGA	N.C.C	CAA	TITC	አ ጥ C	768
10																	700
10	rne	тте	мес	rne		Asp	птэ	Asp	PIO	250	1111	Arg	Arg	GIII	255	TTE.	
					245					230					233		
	GTC	ΔΤΟ	GAG	ACG	ጥሮል	GAA	ССТ	TTC	ACC	AAG	CTC	ACC	СТС	АСТ	GCC	GCG	816
						-						Thr					
15				260					265	-1-				270			
	CAC	CTA	GTT	TTC	GTT	GGA	AA:C	TCT	TCA	GCA	GCT	TCG	GGT	ATA	ACA	GCA	864
	His	Leu	Val	Phe	Val	Gly	Asn	Ser	Ser	Ala	Ala	Ser	Gly	Ile	Thr	Ala	
			275			_		280					285				
20																	
	ACA	TTT	GCC	AGC	AAC	GTG	AAG	CCT	GGA	GAT	ACA	GTT	TTA	GTG	TGG	GAA	912
	Thr	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Asp	Thr	Val	Leu	Val	Trp	Glu	
		290					295					300					
25	GAC	ACA	TGC	GAG	AGC	CTC	AAG	AGC	GTT	ACA	GTG	AAA	AGG	ATT	TAC	ACT	960
	Asp	Thr	Cys	Glu	Ser	Leu	Lys	Ser	Val	Thr	Val	Lys	Arg	Ile	Tyr	Thr	
	305					310					315					320	
	GAG	GAG	CAC	GAG	GGC	TCT	TTT	GCG	CCA	GTC	ACC	.GCG	CAC	GGA	ACC	ATA	1008
30	Glu	Glu	His	Glu	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	
					325					330					335		
	ATA	GTG	GAT	CAG	GTG	TTG	GCA	TCG	TGC	TAC	GCG	GTC	ATT	GAG	AAC	CAC	1056
	Ile	Val	Asp	Gln	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asn	His	
35				340					345					350			
	AAA	TGG	GCA	CAT	TGG	GCT	TTT	GCG	CCG	GTC	AGG	TTG	TGT	CAC	AAG	CTG	1104
	Lys	Trp		His	Trp	Ala	Phe	Ala	Pro	Val	Arg	Leu		His	Lys	Leu	
			355					360					365				

	ATG	ACG	TGG	CTT	TTT	CCG	GCT	CGT	GAA	TCA	AAC	GTC	AAT	TTT	CAG	GAG	1152
	Met	Thr	Trp	Leu	Phe	Pro	Ala	Arg	Glu	Ser	Asn	Val	Asn	Phe	Gln	Glu	
		370					375					380					
5																	
	GAT	GGT	ATC	CAC	TGG	TAC	TCA	AAT	ATG	CTG	TTT	CAC	ATC	GGC	TCT	TGG	1200
	Asp	Gly	Ile	His	Trp	Tyr	Ser	Asn	Met	Leu	Phe	His	Ile	Gly	Ser	Trp	
	385					390					395					400	
10									CCA								1248
	Leu	Leu	Asp	Arg		Ser	Phe	His	Pro		Gly	Ile	Leu	His		Ser	
					405					410					415		
																	1051
1.5	TGA																1251
15																•	
	(2)	TNIEC	אאמר	rion	EOD	SEO	TD !	vi () • 1 (	<b>.</b>								
	(2)	7145	JINPA	LON	FOR	SEQ	10 1	.10.10	<i>.</i>								•
			(i) \$	SEOUE	ENCE	CHAI	RACTI	ERIST	rics:	:							
20									ino a		5						
				(B)	TYE	PE: a	amino	o ac:	id .			:					
				(D)	TOI	POLO	GY:	linea	ar								
		( i	Li) N	OLEC	CULE	TYPE	E: pi	rote	in								
25																	
		( >	ki) S	SEQUE	ENCE	DESC	CRIP:	CION:	: SEQ	O I D	NO:	1.0:					
•	Met	Val	Glu	Met	Leu	Leu	Leu	Thr	Arg	Ile	Leu	Leu	Val	Gly	Phe	Ile	
30	1				5					10					15		
			•														
	Cys	Ala	Leu		Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro		Arg	Gly	
				20					25					30			
2.5	<b>-</b> 1	63	_	_	_		_	-	-	_	<b></b>	_	-	<b>7</b> . 7 -		<b>7</b>	
35	IIe	GIÀ		Arg	Arg	HIS	Pro		Lys	Leu	Thr	Pro		Ala	Tyr	ьys	
			35					40			,		45				
	Gln	Pho	Tla	Pro	Δεν	V = 1	ΔΊ=	Glu	T.ve	Thr	T.e.ii	Glv	Δla	Ser	Glu	Ara	
	GIII	50	116	ELU	ASII	νал	55	JLU	Lys	TILL	пеи	60	лта	SET	O T Y	111.9	
		50					55					30					

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	Tyr 65	Glu	Gly	Lys	Ile	Thr 70	Arg	Asn	Ser	Glu	Arg 75	Phe	Lys	Glu	Leu	Thr
5	Pro	Asn	Tyr	Asn	Pro 85	Asp	Ile	Ile	Phe	Lys 90	Asp	Glu	Glu	Asn	Thr 95	Gly
10	Ala	Asp	Arg	Leu 100	Met	Thr	Gln	Arg	Cys 105	Lys	Asp	Lys	Leu	Asn 110	Ala	Leu
10	Ala	Ile	Ser 115	Val	Met	Asn	Gln	Trp 120	Pro	Gly	Val	Lys	Leu 125	Arg	Val	Thr
15	Glu	Gly 130	Trp	Asp	Glu	Asp	Gly 135	His	His	Ser	Glu	Glu 140	Ser	Leu	Hi.s	Tyr
	Glu 145	Gly	Arg	Ala	Val	Asp 150	Ile	Thr	Thr	Ser	Asp 155	Arg	Asp	Arg	Ser	Lys 160
20	Tyr	Gly	Met	Leu	Ala 165	Arg	Leu	Ala	Val	Glu 170	Ala	Gly	Phe	Asp	Trp 175	Val
25	Tyr	Tyr	Glu	Ser 180	Lys	Ala	His	Ile	His 185	Cys	Ser	Val	Lys	Ala 190	Glu	Asn
	Ser	Val	Ala 195	Ala	Lys	Ser	Gly	Gly 200	Cys	Phe	Pro	Gly	Ser 205	Ala	Thr	Val
30	His	Leu 210	Glu	His	Gly	Gly	Thr 215	Lys	Leu	Val	Lys	Asp 220	Leu	Ser	Pro	Gly
	Asp 225	Arg	Val	Leu	Ala	Ala 230	Asp	Ala	Asp	Gly	Arg 235	Leu	Leu	Tyr	Ser	Asp 240
35	Phe	Leu	Thr	Phe	Leu 245	Asp	Arg	Met	Asp	Ser 250	Ser	Arg	Lys	Leu	Phe 255	Tyr
	Val	Ile	Glu	Thr 260	Arg	Gln	Pro	Arg	Ala 265	Arg	Leu	Leu	Leu	Thr 270	Ala	Ala

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His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly
		275					280					285			

- 5 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln 290 295 300
  - Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser 305 310 315 320

Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro 325 330 335

Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys

340
345
350

Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro 355 360 365

20 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala 370 375 380

Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg 385 390 395 400

Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
405 410 415

Pro Leu Gly Met Val Ala Pro Ala Ser 30 420 425

### (2) INFORMATION FOR SEQ ID NO:11:

- 35 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: protein

5		(2	ki) :	SEQUI	ENCE	DES	CRIP:	rion:	: SE	Q ID	NO:	11:				
	Met 1	Ala	Leu	Pro	Ala 5	Ser	Leu	Leu	Pro	Leu 10	Cys	Суѕ	Leu	Ala	Leu 15	Leu
10	Ala	Leu	Ser	Ala 20	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val 30	Gly	Arg
15	Arg	Arg	Tyr 35	Val	Arg	Lys	Gln	Leu 40	Val	Pro	Leu	Leu	Tyr 45	Lys	Gln	Phe
13	Val	Pro 50	Ser	Met	Pro	Glu	Arg 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Pro	Ala	Glu
20	Gly 65	Arg	Val	Thr	Arg	Gly 70		Glu	Arg	Phe	Arg 75	Asp	Leu	Val	Pro	Asn 80
	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Ser	Gly	Ala 95	Asp
25	Arg	Leu	Met	Thr 100	Glu	Arg	Cys	Lys	Glu 105	Arg	Val	Asn	Ala	Leu 110	Ala	Ile
20	Ala	Val	Met 115	Asn	Met	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
30	Trp	Asp 130	Glu	Asp	Gly	His	His 135	Ala	Gln	Asp	Ser	Leu 140	His	Tyr	Glu	Gly
35	Arg 145	Ala	Leu	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Asn	Lys	Tyr	Gly 160
	Leu	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Tyr

	Glu	Ser	Arg	Asn 180	His	Ile	His	Val	Ser 185	Val	Lys	Ala	Asp	Asn 190	Ser	Leu
5	Ala	Val	Arg 195	Ala	Gly	Gly	Cys	Phe 200	Pro	Gly	Asn	Ala	Thr 205	Val	Arg	Leu
	Arg	Ser 210	Gly	Glu	Arg	Lys	Gly 215	Leu	Arg	Glu	Leu	His 220	Arg	Gly	Asp	Trp
10	Val 225	Leu	Ala	Ala	Asp	Ala 230	Ala	Gly	Arg	Val	Val 235	Pro	Thr	Pro	Val	Leu 240
15	Leu	Phe	Leu	Asp	Arg 245	Asp	Leu	Gln	Arg	Arg 250	Ala	Ser	Phe	Val	Ala 255	Val
	Glu	Thr	Glu	Arg 260	Pro	Pro	Arg	Lys	Leu 265	Leu	Leu	Thr	Pro	Trp 270	His	Leu
20	Val	Phe	Ala 275	Ala	Arg	Gly	Pro	Ala 280	Pro	Ala	Pro	Gly	Asp 285	Phe	Ala	Pro
	Val	Phe 290	Ala	Arg	Arg	Leu	Arg 295	Ala	Gly	Asp	Ser	Val 300	Leu	Ala	Pro	Gly
25	Gly 305	Asp	Ala	Leu	Gln	Pro 310	Ala	Arg	Val	Ala	Arg 315	Val	Ala	Arg	Glu	Glu 320
30	Ala	Val	Gly	Val	Phe 325	Ala	Pro	Leu	Thr		His	Gly	Thr	Leu	Leu 335	
	Asn	Asp	Val	Leu 340	Ala	Ser	Cys	Tyr	Ala 345	Val	Leu	Glu	Ser	His 350	Gln	Trp
35	Ala	His	Arg 355	Ala	Phe	Ala	Pro	Leu 360	Arg	Leu	Leu	His	Ala 365	Leu	Gly	Ala
	Leu	Leu 370	Pro	Gly	Gly	Ala	Val 375	Gln	Pro	Thr	Gly	Met 380	His	Trp	Tyr	Ser

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Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly 385 390 395 (2) INFORMATION FOR SEQ ID NO:12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 411 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu 10 Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg 20 25 30 Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala 35 40 45 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser 50 55 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn 90 85 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg

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			115					120					125			
5	Val	Thr 130	Glu	Gly	Arg	Asp	Glu 135	Asp	Gly	His	His	Ser 140	Glu	Glu	Ser	Leu
3	His 145	Tyr	Glu	Gly	Arg	Ala 150	Val	Asp	Ile	Thr	Thr 155	Ser	Asp	Arg	Asp	Arg 160
10	Asn	Lys	Tyr	Gly	Leu 165	Leu	Ala	.Arg	Leu	Ala 170	Val	Glu	Ala	Gly	Phe 175	Asp
	Trp	Val	Tyr	Tyr 180	Glu	Ser	Lys	Ala	His 185	Val	His	Суз	Ser	Val 190	Ly.s	Ser
15	Glu	His	Ser 195	Ala	Ala	Ala	Lys	Thr 200	Gly	Gly	Cys	Phe	Pro 205	Ala	Gly	Ala
20	Gln	Val 210	Arg	Leu	Glu	Asn	Gly 215	Glu	Arg	Val	Ala	Leu 220	Ser	Ala	Val	Lys
	Pro 225	Gly	Asp	Arg	Val	Leu 230	Ala	Met	Gly	Glu	Asp 235	Gly	Thr	Pro	Thr	Phe 240
25	Ser	Asp	Val	Leu	Ile 245	Phe	Leu	Asp	Arg	Glu 250	Pro	Asn	Arg	Leu	Arg 255	Ala
	Phe	Gln	Val	Ile 260	Glu	Thr	Gln	Asp	Pro 265	Pro	Arg	Arg	.Leu	Ala 270	Leu	Thr
30	Pro	Ala	His 275	Leu	Leu	Phe	Ile	Ala 280	Asp	Asn	His	Thr	Glu 285	Pro	Ala	Ala
35	His	Phe 290	Arg	Ala	Thr	Phe	Ala 295	Ser	His	Val	Gln	Pro 300	Gly	Gln	Tyr	Val
	Leu 305	Val	Ser	Gly	Val	Pro 310	Gly	Leu	Gln	Pro	Ala 315	Arg	Val	Ala	Ala	Val 320
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	_	Ala 36/61		Leu	Thr	Arg	His	Gly

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser (2) INFORMATION FOR SEQ ID NO:13: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Met Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly 

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Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe

			35					40					45			
5	Ile	Pro 50	Asn	Val	Ala	Glu	Lys 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Arg	Tyr	Glu
J	Gly 65	Lys	Ile	Thr	Arg	Asn 70	Ser	Glu	Arg	Phe	Lys 75	Glu	Leu	Thr	Pro	Asr
10	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Thr	Gly	Ala 95	Asp
	Arg	Leu	Met.	Thr 100	Gln	Arg	Cys	Lys	Asp 105	Lys	Leu	Asn	Ala	Leu 110	Ala	T.1 e
15	Ser	Val	Met 115	Asn	Gln	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
20	Trp	Asp	Glu	Asp	Gly	His	His 135	Ser	Glu	Glu	Ser	Leu 140	His	Tyr	Glu	Glγ
	Arg 145	Ala	Val	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Ser	Lys	Tyr	Gl <sub>y</sub> 160
25	Met	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Туг
	Glu	Ser	Lys	Ala 180	His	Ile	His	Cys	Ser 185	Val	Lys	Ala	Glu	Asn 190	Ser	Val
30	Ala	Ala	Lys 195	Ser	Gly	Gly	Cys	Phe 200	Pro	Gly	Ser	Ala	Thr 205	Val	His	Leu
35	Glu	Gln 210	Gly	Gly	Thr	Lys	Leu 215	Val	Lys	Asp	Leu	Arg 220	Pro	Gly	Asp	Arg
-	Val 225	Leu	Ala	Ala	Asp	Asp 230	Gln	Gly	Arg	Leu	Leu 235	Tyr	Ser	Asp	Phe	Leu 240
	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly		Lys 38/61		Val	Phe	Tyr	Val	Ile

					245					250					255	
5	Glu	Thr	Leu	Glu 260	Pro	Arg	Glu	Arg	Leu 265	Leu	Leu	Thr	Ala	Ala 270	His	Leu
3	Leu	Phe	Val 275	Ala	Pro	His	Asn	Asp 280	Ser	Gly	Pro	Thr	Pro 285	Gly	Pro	Ser
10	Ala	Leu 290	Phe	Ala	Ser	Arg	Val 295	Arg	Pro	Gly	Gln	Arg 300	Val	Tyr	Val	Val
	Ala 305	Glu	Arg	Gly	Gly	Asp 310	Arg	Arg	Leu	Leu	Pro 315	Ala	Ala	Val	His	Ser 320
15	Val	Thr	Leu	Arg	Glu 325	Glu	Glu	Ala	Gly	Ala 330	Tyr	Ala	Pro	Leu	Thr 335	Ala
20	His	Gly	Thr	Ile 340	Leu	Ile	Asn	Arg	Val 345	Leu	Ala	Ser	Cys	Tyr 350	Ala	Val
	Ile	Glu	Glu 355	His	Ser	Trp	Ala	His 360	Arg	Ala	Phe	Ala	Pro 365	Phe	Arg	Leu
25	Ala	His 370	Ala	Leu	Leu	Ala	Ala 375	Leu	Ala	Pro	Ala	Arg 380	Thr	Asp	Gly	Gly
	Gly 385	Gly	Gly	Ser	Ile	Pro 390	Ala	Ala	Gln	Ser	Ala 395	Thr	Glu	Ala	Arg	Gly 400
30	Ala	Glu	Pro	Thr	Ala 405	Gly	Ile	His	Trp	Tyr 410	Ser	Gln	Leu	Leu	Tyr 415	His
35	Ile	Gly	Thr	Trp 420	Leu	Leu	Asp	Ser	Glu 425	Thr	Met	His	Pro	Leu 430	Gly	Met
	Ala	Val	Lys 435	Ser	Ser											

## (2) INFORMATION FOR SEQ ID NO:14:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

15

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser

1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

20 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

25

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr 65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
30 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp 115
120
125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg 130 135 140

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145 150 155  Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr T 165 170 1  Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser V 180 185 190	160 Cyr Glu .75
165 170 1 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser V	_
165 170 1 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser V	_
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser V	.75
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser V	
	7-1 71-
180 185 190	ai Aia
10	
Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser I	eu Gln
195 200 205	
Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp I	ys Val
15 210 215 220	
Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe I	le Met
225 230 235	240
20 Fhe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val I	le Glu
245 250 2	255
Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His I	.eu Leu
260 265 270	
25	
Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr A	la Ala
275 280 285	
Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val A	sp Asp
<b>30</b> 290 295 300	
Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr G	ilu Glu
305 310 315	320
303	320
	7-1 77-7
35 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile V	
325 330 3	35
Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln G	ly Leu

	Ala	His	Leu 355	Ala	Phe	Ala	Pro	Ala 360	Arg	Leu	Tyr	Tyr	Tyr 365	Val	Ser	Ser
5	Phe	Leu 370	Ser	Pro	Lys	Thr	Pro 375	Ala	Val	Gly	Pro	Met 380	Arg	Leu	Tyr	Asn
10	Arg 385	Arg	Gly	Ser	Thr	Gly 390	Thr	Pro	Gly	Ser	Cys 395	His	Gln	Met	Gly	Thr 400
	Trp	Leu	Leu	Asp	Ser 405	Asn	Met	Leu	His	Pro 410	Leu	Gly	Met	Ser	Val 415	Asn
15	Ser	Ser														
	(2)	INFO	ORMA	rion	FOR	SEQ	I DI	NO:1	5:							
20			(i) S	(A)	) LE1 ) TY1		: 475 amino	ā am: o ac:			5					
25		. ( :	ii) P	MOLEC	CULE	ТҮР!	E: pı	rote	in							
30		(2	ki) S	SEQUE	ENCE	DES	CRIP.	rion:	: SEÇ	O ID	NO:	15:				
	Met 1	Leu	Leu	Leu	Ala 5	Arg	Cys	Leu	Leu	Leu 10	Val	Leu	Val	Ser	Ser 15	Leu
35	Leu	Val	Cys	Ser 20	Gly	Leu	Ala	Cys	Gly 25	Pro	Gly	Arg	Gly	Phe 30	Gly	Lys
	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile

40

45

	Pro	Asn 50	Val	Ala	Glu	Lys	Thr 55	Leu	Gly	Ala	Ser	Gly 60	Arg	Tyr	Glu	Gly
5	Lys 65	Ile	Ser	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80
	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg
10	Leu	Met	Thr	Gln 100	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ala	Leu	Ala 110	Ile	Ser
15	Val	Met	Asn 115	Gln	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp
	Asp	Glu 130	Asp	Gly	His	His	Ser 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg
20	Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Arg 155	Ser	Lys	Tyr	Gly	Met 160
	Leu	Ala	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu
25	Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala
30	Ala	Lys	Ser 195	Gly	Gly	Cys	Phe		Gly		Ala	Thr	Val 205	His	Leu	Glu
	Gln	Gly 210	Gly	Thr	Lys	Leu	Val 215	Lys	Asp	Leu	Ser	Pro 220	Gly	Asp	Arg	Val
35	Leu 225	Ala	Ala	Asp	Asp	Gln 230	Gly	Arg	Leu	Leu	Tyr 235	Ser	Asp	Phe	Leu	Thr 240
	Phe	Leu	Asp	Arg	Asp 245	Asp	Gly	Ala	Lys	Lys 250	Val	Phe	Tyr	Val	Ile 255	Glu

	Thr	Arg	Glu	Pro 260	Arg	Glu	Arg	Leu	Leu 265	Leu	Thr	Ala	Ala	His 270	Leu	Leu
5	Phe	Val	Ala 275	Pro	His	Asn	Asp	Ser 280	Ala	Thr	Gly	Glu	Pro 285	Glu	Ala	Ser
	Ser	Gly 290	Ser	Gly	Pro	Pro	Ser 295	Gly	Gly	Ala	Leu	Gly 300	Pro	Arg	Ala	Leu
10	Phe 305	Ala	Ser	Arg	Val	Arg 310	Pro	Gly	Gln	Arg	Val 315	Tyr	Val	Val	Ala	Glu 320
15	Arg	Asp	Gly	Asp	Arg 325	Arg	Leu	Leu	Pro	Ala 330	Ala	Val	His	Ser	Val 335	Thr
	Leu	Ser	Glu	Glu 340	Ala	Ala	Gly	Ala	Tyr 345	Ala	Pro	Leu	Thr	Ala 350	Gln	Gly
20-	Thr	Ile	Leu 355	Ile	Asn	Arg	Val	Leu 360	Ala	Ser	Суз	Туг	Ala 365	Val.	Ile	Glu
	Glu	His 370	Ser	Trp	Ala	His	Arg 375	Ala	Phe	Ala	Pro	Phe 380	Arg	Leu	Ala	His
25	Ala 385	Leu	Leu	Ala	Ala	Leu 390	Ala	Pro	Ala	Arg	.Thr 395	Asp	Arg	Gly	Gly	Asp 400
30	Ser	Gly	Gly	_	Asp 405	_		Gly							Leu 415	
	Ala	Pro	Gly	Ala 420	Ala	Asp	Ala	Pro	Gly 425	Ala	Gly	Ala	Thr	Ala 430	Gly	Ile
35	His	Trp	Tyr 435	Ser	Gln	Leu	Leu	Tyr 440	Gln	Ile	Gly	Thr	Trp 445	Leu	Leu	Asp
	Ser	Glu 450	Ala	Leu	His	Pro	Leu 455	Gly	Met	Ala	Val	Lys 460	Ser	Ser	Xaa	Ser

10

.20

25

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala 470 475 465 (2) INFORMATION FOR SEQ ID NO:16: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 411 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu 1 10 Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Fro Gly Arg 20 25 Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala 45 35 40 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser 50 60 55 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu 65 70 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn 85 90

35

100

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg 115 120 125

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn

105

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu

110

		130					135					140				
5	His 145	Tyr	Glu	Gly	Arg	Ala 150	Val	Asp	Ile	Thr	Thr 155	Ser	Asp	Arg	Asp	Arg 160
J	Asn	Lys	Tyr	Gly	Leu 165	Leu	Ala	Arg	Leu	Ala 170	Val	Glu	Ala	Gly	Phe 175	Asp
10	Trp	Val	Tyr	Tyr 180	Glu	Ser	Lys	Ala	His 185	Val	His	Cys	Ser	Val 190	Lys	Ser
	Glu	His	Ser 195	Ala	Ala	Ala	Lys	Thr 200	Gly	Gly	Cys	Phe	Pro 205	Ala	Gly	Ala
15	Gln	Val 210	Arg	Leu	Glu	Ser	Gly 215	Ala	Arg	Va.l	Ala	Leu 220	Ser	Ala	Val	Arg
20	Pro 225	Gly	Asp	Arg	Val	Leu 230	Ala	Met	Gly	Glu	Asp 235	Gly	Ser	Pro	Thr	Phe 240
	Ser	Asp	Val	Leu	Ile 245	Phe	Leu	Asp	Arg	Glu 250	Pro	His	Arg	Leu	Arg 255	
25	Phe	Gln	Val	Ile 260	Glu	Thr	Gln	Asp	Pro 265	Pro	Arg	Arg	Leu	Ala 270	Leu	Thr
	Pro	Ala	His 275	Leu	Leu	Phe	Thr	Ala 280	Asp	Asn	His	Thr	Glu 285	Pro	Ala	Ala
30	Arg	Phe 290	Arg	Ala	Thr	Phe	Ala 295	Ser	His	Val	Gln	Pro 300	Gly	Gln	Tyr	Val
35	Leu 305	Val	Ala	Gly	Val	Pro 310	Gly	Leu	Gln	Pro	Ala 315	Arg	Val	Ala	Ala	Val 320
	Ser	Thr	His	Val	Ala 325	Leu	Gly	Ala	Tyr	Ala 330	Pro	Leu <sub>.</sub>	Thr	Lys	His 335	Gly
	Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser 46/61		Phe	Ala	Ala	Val	Ala

				340					345					350		
5	Asp	His	His 355	Leu	Ala	Gln	Leu	Ala 360	Phe	Trp	Pro	Leu	Arg 365	Leu	Phe	His
J	Ser	Leu 370	Ala	Trp	Gly	Ser	Trp 375	Thr	Pro	Gly	Glu	Gly 380	Val	His	Trp	Tyr
10	Pro 385	Gln	Leu	Leu	Tyr	Arg 390	Leu	Gly	Arg	Leu	Leu 395	Leu	Glu	Glu	Gly	Ser 400
	Phe	His	Pro	Leu	Gly 405	Met	Ser	Gly	Ala	Gly 410	Ser					
15	(2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	NO:1	7:							
			(i) S													
										acids	3					
20				(D)	) TOI	POLOG	GY: J	linea	ar							
		( ±	ii) ñ	MOLE	CULE	TYP	E: pi	rote	ln							
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 amino acids  (B) TYPE: amino acid  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:															
25	Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
	1				5					10					15	
30	Ala	Leu	Pro	Ala 20	Gln	Ser	Cys	Gly	Pro 25	Gly	Arg	Gly	Pro	Val 30	Gly	Arg
	Arg	Arg	Tyr 35	Ala	Arg	Lys	Gln	Leu 40	Val	Pro	Leu	Leu	Tyr 45		Gln	Phe
35	Val	Pro 50	Gly	Val	Pro	Glu	Arg 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Pro	Ala	Glu
	Gly 65	Arg	Val	Ala	Arg	Gly 70	Ser	Glu	Arg	Phe	Arg 75	Asp	Leu	Val	Pro	Asn 80

	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Ser	Gly	Ala 95	Asp
5	Arg	Leu	Met	Thr 100	Glu	Arg	Cys	Lys	Glu 105	Arg	Val	Asn	Ala	Leu 110	Ala	Ile
10	Ala	Val	Met 115	Asn	Met	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
10	Trp	Asp 130	Glu	Asp	Gly	His	His 135	Ala	Gln	Asp	Ser	Leu 140	His	Tyr	Glu	Gly
15	Arg 145	Ala	Leu	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Asn	Lys	Tyr	Gly 160
	Leu	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Tyr
20	Glu	Ser	Arg	Asn 180	His	Val	His	Val	Ser 185	Val	Lys	Ala	Asp	Asn 190	Ser	Leu
25	Ala	Val	Arg 195	Ala	Gly	Gly	Cys	Phe 200	Pro	Gly	Asn	Ala	Thr 205	Val	Arg	Ľeu
25	Trp	Ser 210	Gly	Glu	Arg	Lys	Gly 215	Leu	Arg	Glu	Leu	His 220	Arg	Gly	Asp	Trp
30	Val 225	Leu	Ala	Ala	Asp	Ala 230	Ser	Gly	Arg	Val	Val 235		Thr	Pro	Val	Leu 240
	Leu	Phe	Leu	Asp	Arg 245	Asp	Leu	Gln	Arg	Arg 250	Ala	Ser	Phe	Val	Ala 255	Val
35	Glu	Thr	Glu	Trp 260	Pro	Pro	Arg	Lys	Leu 265	Leu	Leu	Thr	Pro	Trp 270	His	Leu
	Val	Phe	Ala 275	Ala	Arg	Gly	Pro	Ala 280	Pro	Ala	Pro	Gly	Asp 285	Phe	Ala	Pro

	Val	Phe 290	Ala	Arg	Arg	Leu	Arg 295	Ala	Gly	Asp	Ser	Val 300	Leu	Ala	Pro	Gly
5	Gly 305	Asp	Ala	Leu	Arg	Pro 310	Ala	Arg	Val	Ala	Arg 315	Val	Ala	Arg	Glu	Glu 320
10	Ala	Val	Gly	Val	Phe 325	Ala	Pro	Leu	Thr	Ala 330	His	Gly	Thr	Leu	Leu 335	Val
	Asn	Asp	Val	Leu 340	Ala	Ser	Cys	Tyr	Ala 345	Val	Leu	Glu	Ser	His 350	Gl'n	Trp
15	Ala	His	Arg 355	Ala	Phe	Ala	Pro	Leu 360	Arg	Leu	Leu	His	Ala 365	Leu	Gly	Ala
	Leu	Leu 370	Pro	Gly	Gly	Ala	Val 375	Gln	Pro	Thr	Gly	Met: 380	His	Trp	Tyr	Ser
20	Arg 385	Leu	Leu	Tyr	Arg	Leu 390	Ala	Glu	Glu	Leu	Leu 395	Gly				
25	(2)	INFO	ORMAT	LION	FOR	SEQ	ID 1	NO:18	3:							
			(i) S		LEI	IGTH:	: 416	ERIST 5 ami	ino a		5					
30				(D)	TOE	POLOG	GY: ]	Linea	ar							
		, :	: -: \ \ \	AOT EZ	ם ווזי	TVDE	· ~	cot o i								

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly

				20					25					30		
	Tyr	Gly	Lys 35	Arg	Arg	His	Pro	Lys 40	Lys	Leu	Thr	Pro	Leu 45	Ala	Tyr	Lys
5	Gln	Phe 50	Ile	Pro	Asn	Val	Ala 55	Glu	Lys	Thr	Leu	Gly 60	Ala	Ser	Gly	Lys
10	Tyr 65	Glu	Gly	Lys	Ile	Thr 70	Arg	Asn	Ser	Glu	Arg 75	Phe	Lys	Glu	Leu	Ile 80
	.Pro	Asn	Tyr	Asn	Pro 85	Asp	Ile	Ile	Phe	Lys 90	Asp	Glu	Glu	Asn	Thr 95	Asn
1.5	Ala	Asp	Arg	Leu 100	Met	Thr	Lys	Arg	Cys 105	Lys	Asp	Lys	Leu	Asn 110	Ser	Leu
20	Ala	Ile	Ser 115	Va.l	Met	Asn	His	Trp 120	Pro	Gly	Val	Lys	Leu 125	Arg	Val	Thr
	Glu	Gly 130	Trp	Asp	Glu	Asp	Gly 135	His	His	Leu	Glu	Glu 140	Ser	Leu	His	Tyr
25	Glu 145	Gly	Arg	Ala	Val	Asp 150	Ile	Thr	Thr	Ser	Asp 155	Arg	Asp	Lys	Ser	Lys 160
	Tyr	Gly	Met	Leu	Ser 165	Arg	Leu	Ala	Val	Glu 170	Ala	Gly	Phe	Asp	Trp 175	Val
30	Tyr	Tyr	Glu	Ser 180	Lys	Ala	His	Ile	His 185	Cys	Ser	Val	Lys	Ala 190	Glu	Asn
35	Ser	Val	Ala 195	Ala	Lys	Ser	Gly	Gly 200	Cys	Phe	Pro	Gly	Ser 205	Gly	Thr	Val
	Thr	Leu 210	Gly	Asp	Gly	Thr	Arg 215	Lys	Pro	Ile	Lys	Asp 220	Leu	Lys	Val	Gly
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Glu	Lys	Gly	Asn	Val	Leu	Ile	Ser	Asp

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	225					230					235					240
5	Phe	Ile	Met	Phe	Ile 245	Asp	His	Asp	Pro	Thr 250	Thr	Arg	Arg	Gln	Phe 255	Ile
J	Val	Ile	Glu	Thr 260	Ser	Glu	Pro	Phe	Thr 265	Lys	Leu	Thr	Leu	Thr 270	Ala	Ala
10	His	Leu	Val 275	Phe	Val	Gly	Asn	Ser 280	Ser	Ala	Ala	Ser	Gly 285	Ile	Thr	Ala
	Thr	Phe 290	Ala	Ser	Asn	Val	Lys 295	Pro	Gly	"Asp	Thr	Val 300	Leu	Val	Trp	Glu
15	Asp 305	Thr	Cys	Glu	Ser	Leu 310	Lys	Ser	Val	Thr	Val 315	Lys	Arg	Ile	Tyr	Thr 320
20	Glu	Glu	His	Glu	Gly 325	Ser	Phe	Ala	Pro	Val 330		Ala	His	Gly	Thr 335	Ile
20	Ile	Val	Asp	Gln 340	Val	Leu	Ala	Ser	Cys 345	Tyr	Ala	Val	Ile	Glu 350	Asn	His
25	Lys	Trp	Ala 355	His	Trp	Ala	Phe	Ala 360	Pro	Val	Arg	Leu	Cys 365	His	Lys	Leu
	Met	Thr 370	Trp	Leu	Phe	Pro	Ala 375	Arg	Glu	Ser	Asn	Val 380	Asn	Phe	Gln	Glu
30	Asp 385	Gly	Ile	His	Trp	Tyr 390	Ser	Asn	Met	Leu	Phe 395	His	Ile	Gly	Ser	Trp 400
35	Leu	Leu	Asp	Arg	Asp 405	Ser	Phe	His	Pro	Leu 410	Gly	Ile	Leu	His	Leu 415	Ser

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

	(D) MVDD, muslain said																
	(B) TYPE: nucleic acid (C) STRANDEDNESS: both																
			(	C) S'	TRAN	DEDN:	ESS:	bot	h								
	(D) TOPOLOGY: linear																
5																	
		(ii	) MO	LECU:	LE T	YPE:	CDN	A									
		(ix	) FE.	ATURI	E:												
10		•			AME/	KEY:	CDS										
					OCAT			1413									
			( )	<i>D</i> , 2.	00111	2011.		1113									
			\ CE	OUTNI	~= D	ECCD:	r DM T	<b>7.17</b> - 1		TD N/	0.10	_					
1.5		(X1	) SE	ŽO E'IM	CE D	LSCR.	IPIT	JN: :	SEQ .	ID NO	J:19	:					
15																	
															GTC		48
	Met	Asp	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr	
	1				5					10					15		
20	TGT	CTC	TCC	CTG	GGA	TGC	CAA	ATG	CCA	CAG	TTC	CAG	TTC	CAG	TTC	CAG	96
	Cys	Leu	Ser	Leu	Gly	Cys	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln	
				20					25					30			
	CTC	CAA	ATC	CGC	AGC	GAG	CTC	CAT	CTC	CGC	AAG	CCC	GCA	AGA	AGA	ACG	144
25	Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr	
			35					40					45				
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															Arg		
30	0111	50	1100	*****9			55			0211	11.29	60	200	001	9	11Cu	
50		30					<b>J</b> J					00					
	7.00	m c m	CITIC	CMC	ccc	CITIC	CEC	CITIC	7 ELC	C TT C	mm.c	000	7 m.C	CITIC	mmm	7.00	240
															TTT		240
		Ser	Leu	Val	Ala		Leu	Leu	11e	Val		Pro	Met	Val	Phe		
	65					70					75					80	
35																	
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	Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	
					85					90					95		

	CGC	AAC	CTG	TAT	CCG	CTG	GTC	CTC	AAG	CAG	ACA	ATT	CCC	AAT	CTA	TCC	336
	Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	
				100					105					110			
5	GAG	TAC	ACG	AAC	AGC	GCC	TCC	GGA	CCT	CTG	GAG	GGT	GTG	ATC	CGT	CGG	384
	Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	
			115					120					125				
	GAT	TCG	CCC	AAA	TTC	AAG	GAC	CTC	GTG	CCC	AAC	TAC	AAC	AGG	GAC	ATC	432
10	Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	
		130					135					140					
			CGT														480
		Phe	Arg	Asp	Glu		Gly	Thr	Gly	Ala	_	Gly	Leu	Met	Ser		
15	145					1.50					155					160	
	000	m.c.c	220	C T C	T 7 C	CITE TO	770	CELC	CITIC	660	ma c	шсс	CITIC	א וווי כי	7 7 C	C D D	E 2 0
			AAG														528
	Arg	Cys	Lys	GIU	-	Leu	Asn	vaı	Leu		Tyr	Ser	vaı	Met	175	61U	
20					165					170					1/5		
20	TI CC	CCC	GGC	አጥሮ	ccc	CIPC	CTC	CTC	7) C C	CAC	ACC.	TGC	CAC	GNG	GNC	ώλ/C	576
																	570
	пр	PIO	Gly	180	Arg	пец	ьец	vaı	185	GIU	ser	115	Asp	190	Азр	ı yı	
				100					100					1.7.2			
25	САТ	CAC	GGC	CAG	GAG	TCG	СТС	CAC	TAC	GAG	.GGC	CGA	GCG	GTG	ACC	ATT	624
			Gly														
			195					200	_		_	,	205				
	GCC	ACC	TCC	GAT	CGC	GAC	CAG	TCC	AAA	TAC	GGC	ATG	CTC	GCT	CGC	CTG	672
30	Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu	
		210					215					220					
	GCC	GTC	GAG	GCT	GGA	TTC	GAT	TGG	GTC	TCC	TAC	GTC	AGC	AGG	CGC	CAC	720
	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His	
35	225					230					235					240	
	ATC	TAC	TGC	TCC	GTC	AAG	TCA	GAT	TCG	TCG	ATC	AGT	TCC	CAC	GTG	CAC	768
	Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His	
					245					250					255		

	GGC	TGC	TTC	ACG	CCG	GAG	AGC	ACA	GCG	CTG	CTG	GAG	AGT	GGA	GTC	CGG	816
	Gly	Cys	Phe		Pro	Glu	Ser	Thr		Leu	Leu	Glu	Ser	_	Val	Arg	
5				260					265					270			
3	AAG	CCG	CTC	GGC	GAG	CTC	TCT	ATC	GGA	GAT	CGT	GTT	TTG	AGC	ATG	ACC	864
												Val					
			275					280					285				
10												CTC Leu					912
	Ата	290	GIÀ	GIII	Ala	vaı	295	261	Giu	vaı	116	300	FIIC	nec	лър	AIG	
	AAC	CTC	GAG	CAG	ATG	CAA	AAC	TTT	GTG	CAG	CTG	CAC	ACG	GAC	GGT	GGA	960
15		Leu	Glu	Gln	Met		Asn	Phe	Val	Gln		His	Thr	Asp	Gly		
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	Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val	Ser	Val	Trp	Gln	Pro	
20					325					330					3.35		
	07.0	7.00	27.0	220	om o	7.00		OTT C	ar mm	c:cc	C 7 (D	cca	7 m.c	070	C T C	71 7 C	1056
												· CGC				Lys.	1056
	010		0411	340	200		20		345	1120		9		350	014		
25					•												
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	Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro	
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35												Val					1200
	385		_		_	390					395					400	
																,	
												TGG					1248
	Tyr	Ala	Val	ITe	Asn	ser	GIN	ser				Trp	GTA	Leu	Ala	rro	
									4	54/61							

					405					410					415		
				CTG													1296
5	Met	Arg	Leu	Leu 420	Ser	Thr	Leu	GIU	A1a 425	Trp	Leu	Pro	Ala	ьуs 430	GIU	GIN	
3				420					423					430			
	TTG	CAC	AGT	TCG	CCG	AAG	GTG	GTG	AGC	TCG	GCG	CAG	CAG	CAG	AAT	GGC	1344
	Leu	His	Ser	Ser	Pro	Lys	Val	Val	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly	
			435					440					445				
10																	
				TAT													1392
	Ile		Trp	Tyr	Ala	Asn		Leu	Туг	Lys	Vai	Lys 460	Asp	Tyr	Val	Leu	
		450					455					400					
15	CCG	CAG	AGC	TGG	CGC	CAC	GAT	TGA									141.6
	Pro	Gln	Ser	Trp	Arg	His	Asp										
	465					470											
20	100	TNIDO	7 17 N 47 N	TT () AT	EOE	CEO	TD .	10 - 20									
20	(2)	INFO	ORMA'	TION	FOR	SEQ	ID N	10:20	· ):							•	
20	(2)			TION SEQUE						:						• .	
20	(2)			SEQUE	ENCE	СНАГ		ERIST	rics:		6					<b>.</b> .	
20	(2)			SEQUE (A)	ENCE LEI	CHAF	RACTE	ERIST Lami	TICS: ino a		6					· .	
25	(2)			SEQUE (A) (B)	ENCE LEI TYI	CHAF	RACTE	ERIST Lami	rics: ino a		5					٠.	
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			(i) :	SEQUE (A) (B)	ENCE LEI TYI TOI	CHAE NGTH: PE: &	RACTE : 471 amino	ERIST Lami Daci	TICS: ino a id		5						
		į,	(i) :	SEQUE (A) (B)	ENCE LETYI TOI	CHAF NGTH: PE: & POLOC TYPE	RACTE 471 amino GY: 1	ERIST Lami Daci Linea	rics: ino a id ar	aci.ds		20:				• .	
		į,	(i) :	SEQUE (A) (B) (D)	ENCE LETYI TOI	CHAF NGTH: PE: & POLOC TYPE	RACTE 471 amino GY: 1	ERIST Lami Daci Linea	rics: ino a id ar	aci.ds		20:				•	
25		(i	(i) : ii)	SEQUE (A) (B) (D)	ENCE LENCE TYPE TOPE CULE	CHAE NGTH: PE: 6 POLOG TYPE DESC	RACTE: 47] amino GY: ] E: pr	ERIST Lami Daci Linea Cotei	rics: ino a id ar in	acids	NO:2		Ala	Ser	Val	Thr	
25		(i	(i) : ii)	SEQUE (A) (B) (D) MOLEC	ENCE LENCE TYPE TOPE CULE	CHAE NGTH: PE: 6 POLOG TYPE DESC	RACTE: 47] amino GY: ] E: pr	ERIST Lami Daci Linea Cotei	rics: ino a id ar in	acids	NO:2		Ala	Ser	Val 15	Thr	
25	Met 1	(i	(i) : ii) ! ki) :	SEQUE (A) (B) (D) MOLEC	ENCE TYPE TOPE CULE ENCE Ser 5	CHAR NGTH: PE: & POLOC TYPE DESC	RACTE: 471 aminc GY: 1 E: pr CRIPT Val	ERIST Lami Daci Linea rotei TION:	rics: ino a id ar in E SEÇ	Q ID Ala 10	NO:2	Ala			15		
25	Met 1	(i	(i) : ii) ! ki) :	SEQUE (A) (B) (D) MOLEC SEQUE His	ENCE TYPE TOPE CULE ENCE Ser 5	CHAR NGTH: PE: & POLOC TYPE DESC	RACTE: 471 aminc GY: 1 E: pr CRIPT Val	ERIST Lami Daci Linea rotei TION:	rics: ino a id in : SEQ Trp	Q ID Ala 10	NO:2	Ala		Gln	15		
25	Met 1	(i	(i) : ii) ! ki) :	SEQUE (A) (B) (D) MOLEC	ENCE TYPE TOPE CULE ENCE Ser 5	CHAR NGTH: PE: & POLOC TYPE DESC	RACTE: 471 aminc GY: 1 E: pr CRIPT Val	ERIST Lami Daci Linea rotei TION:	rics: ino a id ar in E SEÇ	Q ID Ala 10	NO:2	Ala			15		
25	Met 1 Cys	(i	(i) : ii) ! ki) : Asn	SEQUE (A) (B) (D) MOLEC SEQUE His	ENCE TYPE TOPE CULE ENCE Ser 5	CHAE NGTH: PE: 6 POLOC TYPE DESC Ser Cys	RACTE: 471 amino GY: 1 E: pr CRIPT Val Gln	ERIST Lami Daci Linea Totei TION: Pro	rics: ino a id ar in Trp Pro 25	Q ID Ala 10 Gln	NO:2 Ser Phe	Ala Gln	Phe	Gln 30	15 Phe	Gln	

		Gln	Thr 50	Met	Arg	His	Ile	Ala 55	His	Thr	Gln	Arg	Cys 60	Leu	Ser	Arg	Leu
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	15	Glu	Tyr	Thr 115	Asn	Ser	Ala	Ser	Gly 120	Pro	Leu	Glu	Gly	Val 125	Ile	Arg	Arg
Amil Amir Bash is is built dim. Amil Amil		Asp	Ser 130	Pro	Lys	Phe	Lys	Asp 135	Leu	Val	Pro	Asn	Tyr 140	Asn	Arg	Asp	Ile
	20	Leu 145	Phe	Arg	Asp	Glu	Glu 150	Gly	Thr	Gly	Ala	Asp 155	Gly	Leu	Met	Ser	Lys 160
And those that the those that		Arg	Cys	Lys	Glu	Lys 165	Leu	Asn	Val	Leu	Ala 170	Туг	Ser	Val	Met	Asn 175	Glu
	25	Trp	Pro	Gly	Ile 180	Arg	Leu	Leu	Val	Thr 185	Glu	Ser	Trp	Asp	Glu 190	Asp	Tyr
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15	Ala	Val	Leu	Thr	Val 325	Thr	Pro	Ala	His	.Leu 330	Val	Ser	Val	Trp	Gln 335	Pro
	Glu	Ser	Gln	Lys 340	Leu	Thr	Phe	Val	Phe 345	Ala	His	Arg	Ile	Glu 350	Glu	Lys
20	Asn	Gl.n	Val 355	Leu	Val.	Arg	Asp	Val 360	Glu	Thr	Gly	Glu	Leu 365	Arg	Pro	Gln
	Arg	Val 370	Val	Lys	Leu	Gly	Ser 375	Val	Arg	Ser	Lys	Gly 380	Val	Val	Ala	Pro
25	Leu 385	Thr	Arg	Glu	Gly	Thr 390	Ile	Val	Val	Asn	Ser 395	Val	Ala	Ala	Ser	Cys 400
30	Tyr	Ala	Val	Ile	Asn 405	Ser	Gln	Ser	Leu	Ala 410	His	Trp	Gly	Leu	Ala 415	Pro
50	Met	Arg	Leu	Leu 420	Ser	Thr	Leu •	Glu	Ala 425	Trp	Leu	Pro	Ala	Lys 430	Glu	Gln
35	Leu	His	Ser 435	Ser	Pro	Lys	Val	Val 440	Ser	Ser	Ala	Gln	Gln 445	Gln	Asn	Gly
	Ile	His 450	Trp	Tyr	Ala	Asn	Ala 455	Leu	Tyr	Lys	Val	Lys 460	Asp	Tyr	Val	Leu

Pro Gln Ser Trp Arg His Asp 465 470

(2) INFORMATION FOR SEQ ID NO:21:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

15

20

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Leu

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Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys 50 55 60

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa 100 105 110

35

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser 115 120 125 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu 5 130 135 140 Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys 145 150 155 160 10 Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe 165 170 175 Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Kaa Gly Gly Xaa Lys Xaa Val 180 185 190 15 Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Kaa Gly 195 200 205 Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg 210 215 220 20 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

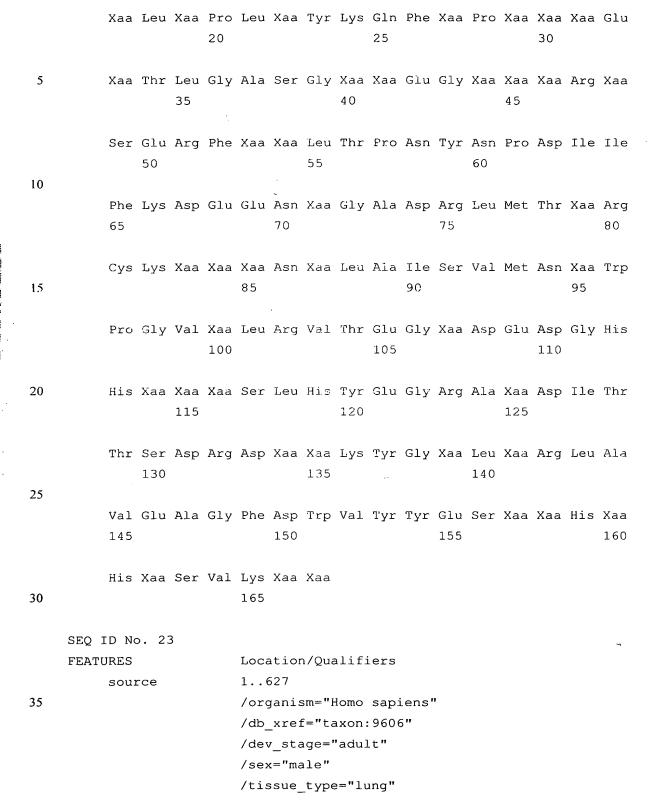
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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60/61

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            61 tgctgctgct ttttgttgct gttcttggtg tcttccgtcc ctgtcacctg ccaaqccctt
           121 ggtcaggaca tggtgtcacc agaggccacc aactettett cetecteett etecteet
           181 tocagogogo gaaggoatgt goggagotac aatoacotto aaggagatgt cogotggaga
           241 aagetattet ettteaceaa gtaetttete aagattgaga agaaegggaa ggteageggg
           301 accaagaagg agaactgccc gtacagcatc ctggagataa catcagtaga aatcggagtt
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           421 tatggctcaa aagaatttaa caatgactgt aagctgaagg agaggataga ggaaaatgga
           481 tacaatacet atgeateatt taactggeag cataatggga ggeaaatgta tgtggeattg
           541 aatygaaaag gageteeaag gagaggacag aaaseaegaa ggaaaaaece etetgeteae
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            61 ssagrhvrsy nhlqgdvrwr klfsftkyfl kiekngkvsg tkkencpysi leitsveigv
          121 vavkainsny ylamnkkgkl ygskefnndc klkerieeng yntyasfnwq hngrqmyval
           181 ngkgaprrgq ktrrkntsah flpmvvhs
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